

gnl|CDD|8102, pfam01715, IPPT, IPP transferase. This is a family of IPP transferases EC:2.5.1.8 also known as tRNA delta(2)-isopentenylpyrophosphate transferase. These enzymes modify both cytoplasmic and mitochondrial tRNAs at A(37) to give isopentenyl A(37).

CD-Length = 253 residues, 90.5% aligned  
Score = 173 bits (441), Expect = 3e-44

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Query:  51  MQVYEGLDIITNKVSAQEQRICRHHMISFVDPLVTNYTVVDFRNRATALIEDIFARDKIP  110
Sbjct:  1   MQVYKGM DIGTAKPSLEEREGVPHHLIDILDPTE-YSAAEFQ RDALEAIAEIRARGKIP  59

Query: 111  IVVGGTNYYYIESLLWKVLVNTK PQEMGTEKVIDRKVE--LEKEDGLVLHKRLSQVDPEMA  168
Sbjct:  60  LLVGGTGLYFKALLDGL-----SDTPAADPKVRAKLEEQLLEELGNDYLHAE LASVDPEAA  114

Query: 169  AKLHPHDKRKVARSLQVFEETGISHSEFLHRQHT EGGG PLGGPLKFSNPCILWLHADQA  228
Sbjct: 115  AKIH PNDGRRIVRALEV FYATGKPISEFQKEQKNAL-----PYDIVQIGLARDRE  164

Query: 229  VLDERLDKRVD DMLAAGLLEELRDFHRRYNQKNVSENSQDYQH GIFQSIGFKEFHEY LIT  288
Sbjct: 165  VLHERIARRVDD MLESGLVEEVKALYAQGLNEDL-----PSIRAIGYKEFLLYL--  213

Query: 289  EGKCTLETSNQL LKKG 304
Sbjct: 214  DGECTLEEAIERI IKN 229

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gnl|CDD|405, smart00451, ZnF\_U1, U1-like zinc finger; Family of C2H2-type zinc fingers, present in matrin, U1 small nuclear ribonucleoprotein C and other RNA-binding proteins.

CD-Length = 35 residues, 91.4% aligned  
Score = 37.1 bits (86), Expect = 0.004

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Query: 363  HLC DLC DRIIIGDREWA AHIKSKSHLNQLKKR 394
Sbjct:  4   FYCKLCNVTF TDEISVEAHLKGKKHKKNVKKR 35

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gnl|CDD|8115, pfam01745, IPT, Isopentenyl transferase. Isopentenyl transferase / dimethylallyl transferase synthesises isopentenyladenosine 5'-monophosphate, a cytokinin that induces shoot formation on host plants infected with the Ti plasmid.

CD-Length = 233 residues, only 16.7% aligned  
Score = 36.8 bits (85), Expect = 0.005

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Query: 19  LVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVY EGL 57
Sbjct:  3  LYLIWGATCTGKTAE AIALAKSTGWPVIVLDRVQCCSQL 41

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gnl|CDD|10515, COG0645, COG0645, Predicted kinase [General function prediction only]

CD-Length = 170 residues, only 18.2% aligned  
Score = 36.5 bits (84), Expect = 0.007

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Query: 19  LVVILGATGTGKSTLALQLGQRLGGEIVSAD 49
Sbjct:  3  LVLVGGLP GSGKSTLARGLAELLGAIRLRS D 33

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ACCESSION NUMBER: 2001:784384 SCISEARCH

THE GENUINE ARTICLE: 476WV

TITLE: Regulation of physiological rates in *Caenorhabditis elegans* by a tRNA-modifying enzyme in the mitochondria

AUTHOR: Lemieux J; Lakowski B; Webb A; Meng Y; Ubach A; Bussiere F; Barnes T; Hekimi S (Reprint)

CORPORATE SOURCE: McGill Univ, Dept Biol, 1205 Doctor Penfield Ave, Montreal, PQ H3A 1B1, Canada (Reprint); McGill Univ, Dept Biol, Montreal, PQ H3A 1B1, Canada

COUNTRY OF AUTHOR: Canada

SOURCE: GENETICS, (SEP 2001) Vol. 159, No. 1, pp. 147-157.

Publisher: GENETICS, 428 EAST PRESTON ST, BALTIMORE, MD 21202 USA.

ISSN: 0016-6731.

DOCUMENT TYPE: Article; Journal

LANGUAGE: English

REFERENCE COUNT: 39

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB We show that the phenotype associated with *gro-1*(e2400) comprises the whole suite of features that characterize the phenotype of the *dl* mutants in *Caenorhabditis elegans*, including deregulated developmental, behavioral, and reproductive rates, as well as increased life span and a maternal effect. We cloned *gro-1* and found that it encodes a highly conserved cellular enzyme, isopentenylpyrophosphate:tRNA transferase (IPT), which modifies a subset of tRNAs. In yeast, two forms of the enzyme are produced by alternative translation initiation, one of which is mitochondrial. In the *gro-1* transcript there are also two possible initiator ATGs, between which there is a sequence predicted to encode a mitochondrial localization signal. A functional *GRO-1::GFP* fusion protein is localized diffusely throughout the cytoplasm and nucleus. A *GRO-1::GFP* initiated from the first methionine is localized exclusively to the mitochondria and rescues the mutant phenotype. In contrast, a protein initiated from the second methionine is localized diffusely throughout

the cell and does not rescue the mutant phenotype. As oxygen consumption and ATP concentration have been reported to be unaffected in *gro-1* mutants, our observations suggest that *GRO-1* acts in mitochondria and regulates global physiology by unknown mechanisms.

L4 ANSWER 2 OF 6 SCISEARCH COPYRIGHT 2003 THOMSON ISI

ACCESSION NUMBER: 2002:441430 SCISEARCH

THE GENUINE ARTICLE: 552EV

TITLE: Allelic polymorphisms in the Fc gamma RIIC gene can influence its function on normal human natural killer cells

AUTHOR: Ernst L K; Metes D; Herberman R B; Morel P A (Reprint)

CORPORATE SOURCE: Univ Pittsburgh, Inst Canc, Pittsburgh, PA USA (Reprint); Univ Pittsburgh, Dept Pathol, Pittsburgh, PA USA; Univ Pittsburgh, Dept Surg, Pittsburgh, PA USA; Univ Pittsburgh, Dept Med, Pittsburgh, PA USA; Univ

Pittsburgh,

Dept Mol Genet & Biochem, Pittsburgh, PA USA

COUNTRY OF AUTHOR: USA

SOURCE: JOURNAL OF MOLECULAR MEDICINE-JMM, (APR 2002) Vol. 80, No.

4, pp. 248-257.

Publisher: SPRINGER-VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010 USA.

ISSN: 0946-2716.

DOCUMENT TYPE: Article; Journal

LANGUAGE: English

REFERENCE COUNT: 31

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Natural killer (NK) cells are important in host defense against viruses

and tumors and can induce death of virally infected cells following engagement of cell surface receptors. Human NK cells express receptors for

the Fc portion of IgG which stimulate antibody-dependent cell-mediated cytotoxicity and induce cytokine production. We have shown that NK cells from certain individuals can express, in addition to CD16 (FcgammaRIIIa), isoforms of CD32 (FcgammaRIIc 1-4). Expression of CD32 on NK cells is dependent on an allelic polymorphism of the FcgammaRIIC gene. We analyzed the expression and function of CD32 on NK cells from 31 normal donors. Fourteen of the 31 (45%) donors expressed CD32 on their NK cells. Molecular characterization of FcgammaRIIc isoforms expressed by the CD32(+) donors revealed that the majority of donors expressed the FcgammaRIIc 1 isoform. Interestingly, 3 of the 14 positive donors did not express FcgammaRIIc 1, and we identified a novel isoform, FcgammaRIIc5, expressed by these individuals. The expression of this isoform was correlated to a second allelic polymorphism that controls exon splicing. One of the three was found to express FcgammaRIIb on the NK cells. Biochemical analysis revealed that CD32(+) donors of both types expressed a 40-kDa protein, specifically immunoprecipitated by anti-CD32 monoclonal antibodies. Functionally, only individuals expressing the FcgammaRIIc 1 isoform were able to trigger reverse antibody-dependent cell-mediated cytotoxicity via CD32 whereas a CD32(+) individual expressing the FcgammaRIIb isoform was unable to trigger this function. These results demonstrate that the presence of multiple allelic polymorphisms in the FcgammaRIIC gene determine the expression and function of CD32 on NK cells.



NCBI

# NCBI Conserved Domain Search

PubMed

Nucleotide

Protein

Structure

Taxonomy

RPS-BLAST 2.2.6 [Apr-09-2003]

Query= lcl|tmpseq\_0  
(435 letters)

Database: cdd.v1.62  
11,088 PSSMs; 2,717,223 total columns

Click on boxes for multiple alignments



Show Domain Relatives

PSSMs producing significant alignments:	Score	E value
<a href="#">gnl CDD 10198</a> COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transfer...	226	5e-60
<a href="#">gnl CDD 8102</a> pfam01715, IPPT, IPP transferase. This is a family of IPP tran...	173	3e-44
<a href="#">gnl CDD 405</a> smart00451, ZnF_U1, U1-like zinc finger; Family of C2H2-type z...	37.1	0.004
<a href="#">gnl CDD 8115</a> pfam01745, IPT, Isopentenyl transferase. Isopentenyl transfera...	36.8	0.005
<a href="#">gnl CDD 10515</a> COG0645, COG0645, Predicted kinase [General function predictio...	36.5	0.007

[gnl|CDD|10198](#), COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transferase [Translation, ribosomal structure and biogenesis]

CD-Length = 308 residues, 85.4% aligned  
Score = 226 bits (577), Expect = 5e-60

Query:	18	PLVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVYEGLDIITNKVSAQEQRICRHHMI	77
Sbjct:	4	KLIVIAGPTASGKTALAIALAKRLGGEIISLDSMQVYRGLDIGTAKPSLEELAGVPHHLI	63
Query:	78	SFVDPLVTNYTVVDFRNRATALIEDIFARDKIPIVGGTNYIYESLLWKVLVNTKPPQEMG	137
Sbjct:	64	DIRDP-TESYSAAEFQRDALAAIDDILARGKLPIVGGTGLYLKA-LLEGLSLLPEADPE	121
Query:	138	TEKVIDRKVELEKEDGLVLHKRLSQVDPMAAKLHPHDKRKVARSLQVFEETGISHSEFL	197
Sbjct:	122	VRRRLEA--ELAE LGNDALHAELKKIDPEAAAKIHPNDPQRIIRALEVYYLTGKPISELQ	179
Query:	198	HRQHTTEGGGPLGGPLKFSNPCILWLHADQAVLDERLDKRVDDMLAAGLLEELRDFHRRY	257
Sbjct:	180	KRSRPILEPY-----DILIIALAADREVLIERINRRVDAMLEQGLIEEVKALYARG	230
Query:	258	NQKNVSENSQDYQHGFQSIGFKEFHEYLITEGKCTLETSNQLLKKG	304
Sbjct:	231	LHLD-----LPAMQAIGYKEILAYL--DGGISLEEAIERIKTA	266